

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 08/444,791B
Source: IFW/16
Date Processed by STIC: 10/17/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 10/17/2005

PATENT APPLICATION: US/08/444,791B

TIME: 12:31:09

Input Set : A:\40451c.txt

Output Set: N:\CRF4\10172005\H444791B.raw

3 <110> APPLICANT: Brockhaus, et al.
 5 <120> TITLE OF INVENTION: Human TNF Receptor
 7 <130> FILE REFERENCE: 01017/40451C
 9 <140> CURRENT APPLICATION NUMBER: US 08/444,791B
 10 <141> CURRENT FILING DATE: 1995-05-19
 12 <150> PRIOR APPLICATION NUMBER: US 08/095,640
 13 <151> PRIOR FILING DATE: 1993-07-21
 15 <150> PRIOR APPLICATION NUMBER: US 07/580,013
 16 <151> PRIOR FILING DATE: 1990-09-10
 18 <150> PRIOR APPLICATION NUMBER: CH 1347/90
 19 <151> PRIOR FILING DATE: 1990-04-20
 21 <150> PRIOR APPLICATION NUMBER: CH 746/90
 22 <151> PRIOR FILING DATE: 1990-03-08
 24 <150> PRIOR APPLICATION NUMBER: CH 3319/89
 25 <151> PRIOR FILING DATE: 1989-09-12
 27 <160> NUMBER OF SEQ ID NOS: 26
 29 <170> SOFTWARE: PatentIn version 3.3
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 2111
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens
 36 <400> SEQUENCE: 1
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 39 ccctcaactg tcacccaag gcacttggga cgctcctggac agaccgagtc ccgggaagcc 120
 41 ccagcactgc cgctgccaca ctgccctgag cccaaatggg ggagtgagag gccatagctg 180
 43 tctggcatgg gcctctccac cgtgcctgac ctgctgctgc cgctgggtgct cctggagctg 240
 45 ttggtgggaa tatacccctc aggggttatt ggactggctc ctcacctagg ggacagggag 300
 47 aagagagata gtgtgtgtcc ccaaggaaaa tatatccacc ctcaaaataa ttcgatttgc 360
 49 tgtaccaagt gccacaaagg aacctacttg tacaatgact gtccaggccc ggggcaggat 420
 51 acggactgca gggagtgtga gagcggctcc ttcaccgctt cagaaaacca cctcagacac 480
 53 tgcctcagct gctccaaatg ccgaaaggaa atgggtcagg tggagatctc ttcttgca 540
 55 gtggaccggg acaccgtgtg tggctgcagg aagaaccagt accggcatta ttggagtga 600
 57 aaccttttcc agtgcttcaa ttgcagcctc tgctcctaat ggaccgtgca cctctcctgc 660
 59 caggagaaac agaacaccgt gtgcacctgc catgcagggt tcttttctaag agaaaacgag 720
 61 tgtgtctcct gtagtaactg taagaaaagc ctggagtgca cgaagtgtgt cctaccccag 780
 63 attgagaatg ttaagggcac tgaggactca ggcaccacag tgctgttgcc cctgggtcatt 840
 65 ttcttttggtc ttgctctttt atccctcctc ttcattgggt taatgtatcg ctaccaacgg 900
 67 tggaagtcca agctctactc cattgtttgt gggaaatcga cacctgaaaa agaggggggag 960
 69 cttgaaggaa ctactactaa gccctcggcc ccaaacccaa gcttcagtc cactccaggc 1020
 71 ttcaccccca ccctgggctt cagtcctcgtg ccagttcca ccttcacctc cagctccacc 1080
 73 tatacccccg gtgactgtcc caactttgcg gctccccgca gagaggtggc accaccctat 1140
 75 cagggggctg accccatcct tgcgacagcc ctgcctccg accccatccc caacccctt 1200
 77 cagaagtggg aggacagcgc ccacaagcca cagagcctag acactgatga ccccgcgacg 1260

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79 ctgtacgccg tgggtggagaa cgtgcccccg ttgcgctgga aggaattcgt gcggcgccta 1320
81 gggctgagcg accacgagat cgatcggtcg gagctgcaga acgggcgctg cctgcgcgag 1380
83 gcgcaataca gcatgctggc gacctggagg cggcgcacgc cgcggcgaga ggccacgctg 1440
85 gagctgctgg gacgcgtgct ccgcgacatg gacctgctgg gctgcctgga ggacatcgag 1500
87 gaggcgtttt gcgccccgcg cgccctcccg cccgcgcca gtcttctcag atgaggctgc 1560
89 gcccctgcgg gcagctctaa ggaccgtcct gcgagatcgc cttccaaccc cacttttttc 1620
91 tggaaaggag gggctcctgca ggggcaagca ggagctagca gccgcctact tggtgctaac 1680
93 ccctcgatgt acatagcttt tctcagctgc ctgcgcgcg ccgacagtca gcgctgtgcg 1740
95 cgcgagagaga ggtgcgccgt gggctcaaga gcctgagtgg gtggtttgcg aggatgaggg 1800
97 acgctatgcc tcatgcccgt tttgggtgtc ctcaccagca aggctgctcg ggggcccctg 1860
99 gttcgtccct gagccttttt cacagtgcac aagcagtttt ttttgttttt gttttgtttt 1920
101 gttttgtttt taaatcaatc atgttacact aatagaaact tggcactcct gtgccctctg 1980
103 cctggacaag cacatagcaa gctgaactgt cctaaggcag gggcgagcac ggaacaatgg 2040
105 ggctttcagc tggagctgtg gacttttgta catacactaa aattctgaag ttaaaaaaaa 2100
107 aaccggaatt c 2111
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 455
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 2
117 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
118 1 5 10 15
121 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
122 20 25 30
125 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
126 35 40 45
129 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
130 50 55 60
133 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
134 65 70 75 80
137 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
138 85 90 95
141 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
142 100 105 110
145 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
146 115 120 125
149 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
150 130 135 140
153 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
154 145 150 155 160
157 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
158 165 170 175
161 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
162 180 185 190
165 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
166 195 200 205
169 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
170 210 215 220
173 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys

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174 225          230          235          240
177 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
178          245          250          255
181 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
182          260          265          270
185 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
186          275          280          285
189 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
190          290          295          300
193 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
194 305          310          315          320
197 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
198          325          330          335
201 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
202          340          345          350
205 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
206          355          360          365
209 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
210          370          375          380
213 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
214 385          390          395          400
217 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
218          405          410          415
221 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
222          420          425          430
225 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
226          435          440          445
229 Pro Ala Pro Ser Leu Leu Arg
230          450          455
233 <210> SEQ ID NO: 3
234 <211> LENGTH: 2339
235 <212> TYPE: DNA
236 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 3
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241 cccgagtgtc tgagctgtgg ctcccgtgtg agctctgacc aggtggaaac tcaagcctgc 120
243 actcgggaac agaaccgcat ctgcacctgc agggccggct ggtactgcgc gctgagcaag 180
245 caggaggggt gccggctgtg cgcgcctgtg ccgaagtgcc gcccggtt cggcgtggcc 240
247 agaccaggaa ctgaaacatc agacgtggtg tgcaagccct gtgccccggg gacgttctcc 300
249 aacacgactt catccacgga tatttgcagg cccaccaga tctgtaacgt ggtggccatc 360
251 cctgggaatg caagcaggga tgcagtctgc acgtccacgt ccccccaccg gagtatggcc 420
253 ccaggggcag tacacttacc ccagccagtg tccacacgat cccaacacac gcagccaagt 480
255 ccagaacca gactgtctcc aagcacctcc ttctgtctcc caatgggccc cagcccccca 540
257 gctgaaggga gactggcga ctctgctctt ccagttggac tgattgtggg tgtgacagcc 600
259 ttgggtctac taataatagg agtggtgaac tgtgtcatca tgaccaggt gaaaaagaag 660
261 cccttgtgcc tgcagagaga agccaagggt cctcacttgc ctgccgataa ggccccgggt 720
263 acacagggcc ccgagcagca gcacctgtg atcacagcgc cgagctccag cagcagctcc 780
265 ctggagagct cggccagtgc gttggacaga agggcgccca ctcggaacca gccacaggca 840
267 ccaggcgtgg aggccagtgg ggccggggag gcccgggcca gcaccgggag ctacgcagat 900

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269 tcttcccctg gtggccatgg gaccaggtc aatgtcacct gcatcgtgaa cgtctgtagc 960
271 agctctgacc acagctcaca gtgctcctcc caagccagct ccacaatggg agacacagat 1020
273 tccagcccct cggagtcacc gaaggacgag caggtcccct tctccaagga ggaatgtgcc 1080
275 ttctgggtcac agctggagac gccagagacc ctgctgggga gcaccgaaga gaagcccctg 1140
277 ccccttgagg tgccctgatgc tgggatgaag cccagttaac caggccggtg tgggctgtgt 1200
279 cgtagccaaag gtggctgagc cctggcagga tgacctgcg aaggggccct ggtccttcca 1260
281 ggccccacc actaggactc tgaggctctt tctgggcca gttcctctag tgccctccac 1320
283 agccgcagcc tccctctgac ctgcaggcca agagcagagg cagcgagttg tggaaagcct 1380
285 ctgctgccat ggcgtgtccc tctcggaagg ctggctgggc atggacgttc ggggcatgct 1440
287 ggggcaagtc cctgagtctc tgtgacctgc cccgccagc tgcacctgcc agcctggctt 1500
289 ctggagccct tgggtttttt gttgtttgt ttgtttgtt gttgtttct cccctgggc 1560
291 tctgccagc tctggttcc agaaaacccc agcatcctt tctgcagagg ggctttctgg 1620
293 agaggaggga tgctgcctga gtcacccatg aagacaggac agtgcttcag cctgaggctg 1680
295 agactgcggg atggctcctg ggtctctgtc agggaggagg tggcagccct gtagggaacg 1740
297 gggctccttca agttagctca ggaggcttgg aaagcatcac ctcaggccag gtgcagtggc 1800
299 tcacgcctat gatcccagca ctttgggagg ctgaggcggg tggatcacct gagggttagga 1860
301 gttcgagacc agcctggcca acatggtaaa acccatctc tactaaaaat acagaaatta 1920
303 gccgggcgtg gtggcgggca cctatagtcc cagctactca gaagcctgag gctgggaaat 1980
305 cgtttgaacc cgggaagcgg aggttgacag gagccgagat cagccactg cactccagcc 2040
307 tgggcgacag agcgagagtc tgtctcaaaa gaaaaaaaaa aagcaccgcc tccaaatgct 2100
309 aacttgtcct tttgtacct ggtgtgaaag tcagatgccc agagggccca ggcaggccac 2160
311 catattcagt gctgtggcct gggcaagata acgcattct aactagaaat ctgccattt 2220
313 tttaaaaaag taagtaccac tcaggccaac aagccaacga caaagccaaa ctctgccagc 2280
315 cacatccaac ccccccctg ccatttgcac cctccgcctt cactccggtg tgccctgcag 2339

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318 <210> SEQ ID NO: 4

319 <211> LENGTH: 392

320 <212> TYPE: PRT

321 <213> ORGANISM: Homo sapiens

323 <400> SEQUENCE: 4

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325 Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
326 1 5 10 15
329 Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
330 20 25 30
333 Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
334 35 40 45
337 Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
338 50 55 60
341 Arg Leu Cys Ala Pro Leu Pro Lys Cys Arg Pro Gly Phe Gly Val Ala
342 65 70 75 80
345 Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
346 85 90 95
349 Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
350 100 105 110
353 Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala
354 115 120 125
357 Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
358 130 135 140
361 His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Ser
362 145 150 155 160

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365 Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
366                               165                               170                               175
369 Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val
370                               180                               185                               190
373 Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val
374                               195                               200                               205
377 Val Asn Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu
378                               210                               215                               220
381 Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly
382 225                               230                               235                               240
385 Thr Gln Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser
386                               245                               250                               255
389 Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala
390                               260                               265                               270
393 Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala
394                               275                               280                               285
397 Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Ala Asp Ser Ser Pro Gly
398                               290                               295                               300
401 Gly His Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser
402 305                               310                               315                               320
405 Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met
406                               325                               330                               335
409 Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val
410                               340                               345                               350
413 Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro
414                               355                               360                               365
417 Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val
418                               370                               375                               380
421 Pro Asp Ala Gly Met Lys Pro Ser
422 385                               390

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425 <210> SEQ ID NO: 5

426 <211> LENGTH: 28

427 <212> TYPE: PRT

428 <213> ORGANISM: Artificial sequence

430 <220> FEATURE:

431 <223> OTHER INFORMATION: Synthetic peptide

434 <220> FEATURE:

435 <221> NAME/KEY: misc_feature

436 <222> LOCATION: (25)..(25)

437 <223> OTHER INFORMATION: Xaa = unknown amino acid

439 <400> SEQUENCE: 5

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442 1 5 10 15

W--> 445 Gln Gly Lys Tyr Ile His Pro Glu Xaa Asn Ser Ile

446 20 25

448 <210> SEQ ID NO: 6

449 <211> LENGTH: 15

450 <212> TYPE: PRT

451 <213> ORGANISM: Artificial sequence

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/17/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 25
Seq#:10; Xaa Pos. 8
Seq#:11; Xaa Pos. 2
Seq#:14; Xaa Pos. 9,10,13

VERIFICATION SUMMARY

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L:445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:16
L:524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:601 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0